

Abstract of the disclosure:

Process for finding oligonucleotide sequences for nucleic acid amplification methods

A process for finding heterologous oligonucleotide sequences for a nucleic acid amplification method is described, in which process

- a) mutually overlapping oligonucleotide sequences are generated by fragmenting conserved regions of the target nucleic acid to be amplified,
- b) these sequence fragments are used for finding similar DNA segments in Genbank or other DNA databases and suitable heterologous oligonucleotide sequences which are derived from organisms of other species are thereby identified, and
- c) the heterologous oligonucleotide sequences which have been found are employed as primers and/or probes for isolating the target nucleic acid using a nucleic acid amplification method.